

SCORE Search Results Details for Application 10762888 and Search Result us-10-762-888-10.rag.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10762888 and Search Result us-10-762-888-10.rag.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2006, 05:23:42 ; Search time 200 Seconds
(without alignments)
848.136 Million cell updates/sec

Title: US-10-762-888-10
Perfect score: 2015
Sequence: 1 MNVKGRVLSMLLVSTVMVV.....IRIVKIAWQKKEYNLVRNNI 371

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2015	100.0	371	5	AAE29229 Aae29229 Pig alpha
2	2015	100.0	371	5	AAE16320 Aae16320 Pig alpha
3	2015	100.0	371	6	AAO19634 Aao19634 Porcine a
4	2015	100.0	371	6	ABR81974 Abr81974 Sus scrof
5	2015	100.0	371	7	ABR82709 Abr82709 Porcine a
6	2009	99.7	375	2	AAW49686 Aaw49686 Porcine a
7	2008	99.7	371	5	AAO21516 Aao21516 Pig alpha
8	2004	99.5	371	2	AAR85082 Aar85082 Porcine a
9	1998	99.2	371	2	AAR76777 Aar76777 Pig alpha
10	1925	95.5	359	2	AAR62508 Aar62508 Galactosy

11	1925	95.5	359	2	AAR90573	Aar90573	Pig alpha
12	1923	95.4	363	2	AAW49687	Aaw49687	Porcine a
13	1858.5	92.2	354	2	AAW49688	Aaw49688	Porcine a
14	1779.5	88.3	342	2	AAW49689	Aaw49689	Porcine a
15	1726.5	85.7	376	5	AAO21518	Aao21518	Consensus
16	1723.5	85.5	376	2	AAR80016	Aar80016	Marmoset
17	1723.5	85.5	376	5	AAO21512	Aao21512	Marmoset
18	1723.5	85.5	376	5	AAE16319	Aae16319	Marmoset
19	1717.5	85.2	368	5	AAE29228	Aae29228	Bovine al
20	1717.5	85.2	368	5	AAO21515	Aao21515	Bovine al
21	1717.5	85.2	368	5	AAE16318	Aae16318	Bovine al
22	1717.5	85.2	368	6	AAO19635	Aao19635	Bovine al
23	1717.5	85.2	376	6	AAO19636	Aao19636	Marmoset
24	1711	84.9	369	5	AAE29227	Aae29227	Sheep alp
25	1711	84.9	369	5	AAO21514	Aao21514	Sheep alp
26	1711	84.9	369	5	AAE16317	Aae16317	Sheep alp
27	1711	84.9	369	5	AAE29224	Aae29224	Sheep alp
28	1710.5	84.9	368	5	AAG78468	Aag78468	Predicted
29	1709.5	84.8	376	5	AAO21519	Aao21519	Humanised
30	1697.5	84.2	364	5	AAG78469	Aag78469	Amino aci
31	1578	78.3	418	8	ADQ97726	Adq97726	Mouse can
32	1575	78.2	371	6	AAO19637	Aao19637	Murine al
33	1575	78.2	371	6	ABU79110	Abu79110	Carbohydr
34	1575	78.2	371	7	ADF43354	Adf43354	Carbohydr
35	1575	78.2	371	9	AEA03025	Aea03025	CD14 rece
36	1575	78.2	371	9	AED65395	Aed65395	Mouse alp
37	1510	74.9	359	5	AAO21517	Aao21517	Mouse alp
38	1510	74.9	394	2	AAR13750	Aar13750	GDP-Fuc:[
39	1510	74.9	394	2	AAR45935	Aar45935	A glycosy
40	1510	74.9	394	2	AAW13639	Aaw13639	Murine al
41	1510	74.9	394	5	AAG78483	Aag78483	Murine al
42	1510	74.9	394	5	AAE16321	Aae16321	Mouse alp
43	1510	74.9	394	6	ABG75513	Abg75513	Mouse alp
44	1510	74.9	394	7	ADI39872	Adi39872	Murine al
45	1440	71.5	313	2	AAR62507	Aar62507	Galactosy

ALIGNMENTS

RESULT 1

AAE29229

ID AAE29229 standard; protein; 371 AA.

XX

AC AAE29229;

XX

DT 27-JAN-2003 (first entry)

XX

DE Pig alpha(1,3)galactosyltransferase (alpha1,3GT).

XX

KW Carbohydrate antigen; alpha(1,3)galactosyltransferase; alpha1,3GT; pig;
transgenic; alpha(1,2)fucosyltransferase; alpha1,2FT; enzyme.

XX

OS Sus scrofa.

XX

PN WO200274948-A2.

XX

PD 26-SEP-2002.

XX

PF 21-MAR-2002; 2002WO-CA000378.

XX

PR 21-MAR-2001; 2001US-0277811P.

XX

PA (GERO-) GERON CORP.

XX

PI Denning C, Clark AJ, Schiff JM;

XX

DR WPI; 2002-759895/82.

DR

N-PSDB; AAD46824.

XX

PT Mammalian cells, useful for producing animal tissues with carbohydrate

PT antigens that are compatible for transplantation into human patients.

XX

PS Disclosure; Page 35; 71pp; English.

XX

CC The invention relates to animal tissues with carbohydrate antigens that

SCORE Search Results Details for Application 10762888 and Search Result us-10-762-888-10.ra

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10762888 and Search Result us-10-762-888-10.ra.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2006, 05:33:08 ; Search time 53 Seconds
(without alignments)
612.714 Million cell updates/sec

Title: US-10-762-888-10
Perfect score: 2015
Sequence: 1 MNVKGKRVLSMLLVSTVMVV.....IRIVKIAWQKKEYNLVRNNI 371

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2015	100.0	371	1	US-08-378-617A-10	Sequence 10, Appl
2	2015	100.0	371	2	US-09-994-427A-10	Sequence 10, Appl
3	2015	100.0	371	2	US-08-984-900-10	Sequence 10, Appl
4	1726.5	85.7	376	2	US-09-994-427A-12	Sequence 12, Appl
5	1723.5	85.5	376	1	US-08-704-548-2	Sequence 2, Appli
6	1723.5	85.5	376	2	US-09-173-270-2	Sequence 2, Appli
7	1723.5	85.5	376	2	US-09-994-427A-6	Sequence 6, Appli
8	1723.5	85.5	376	2	US-09-995-419A-9	Sequence 9, Appli
9	1717.5	85.2	368	1	US-08-378-617A-11	Sequence 11, Appl
10	1717.5	85.2	368	2	US-09-994-427A-9	Sequence 9, Appli
11	1717.5	85.2	368	2	US-08-984-900-11	Sequence 11, Appl
12	1711	84.9	369	2	US-09-994-427A-8	Sequence 8, Appli
13	1711	84.9	369	2	US-09-995-419A-7	Sequence 7, Appli

14	1709.5	84.8	376	2	US-09-994-427A-13	Sequence 13, Appl
15	1575	78.2	371	1	US-08-378-617A-12	Sequence 12, Appl
16	1575	78.2	371	2	US-08-984-900-12	Sequence 12, Appl
17	1510	74.9	359	2	US-09-994-427A-11	Sequence 11, Appl
18	1510	74.9	394	1	US-07-914-281-4	Sequence 4, Appli
19	1510	74.9	394	1	US-08-393-246-4	Sequence 4, Appli
20	1510	74.9	394	1	US-08-525-058A-4	Sequence 4, Appli
21	1510	74.9	394	1	US-08-696-731-4	Sequence 4, Appli
22	1510	74.9	394	2	US-09-042-531-4	Sequence 4, Appli
23	1510	74.9	394	2	US-08-379-040-2	Sequence 2, Appli
24	1510	74.9	394	5	PCT-US91-00899-9	Sequence 9, Appli
25	1273	63.2	279	5	PCT-US91-00899-8	Sequence 8, Appli
26	993	49.3	227	2	US-09-994-427A-7	Sequence 7, Appli
27	673	33.4	339	3	US-10-114-270-126	Sequence 126, App
28	644.5	32.0	347	2	US-09-949-016-9849	Sequence 9849, Ap
29	642	31.9	375	1	US-07-752-101A-52	Sequence 52, Appl
30	639	31.7	353	1	US-07-752-101A-35	Sequence 35, Appl
31	639	31.7	353	2	US-09-994-427A-3	Sequence 3, Appli
32	639	31.7	353	2	US-09-995-419A-11	Sequence 11, Appl
33	638.5	31.7	354	1	US-07-752-101A-51	Sequence 51, Appl
34	638.5	31.7	354	2	US-09-994-427A-5	Sequence 5, Appli
35	638.5	31.7	354	2	US-09-995-419A-13	Sequence 13, Appl
36	627.5	31.1	355	2	US-09-949-016-9587	Sequence 9587, Ap
37	623	30.9	353	1	US-07-752-101A-36	Sequence 36, Appl
38	622.5	30.9	354	1	US-07-752-101A-38	Sequence 38, Appl
39	622.5	30.9	354	1	US-07-752-101A-39	Sequence 39, Appl
40	622.5	30.9	354	1	US-07-752-101A-41	Sequence 41, Appl
41	463	23.0	195	1	US-07-752-101A-68	Sequence 68, Appl
42	298.5	14.8	136	2	US-09-621-976-4995	Sequence 4995, Ap
43	297.5	14.8	106	2	US-09-461-325-419	Sequence 419, App
44	297.5	14.8	106	2	US-10-012-542-419	Sequence 419, App
45	297.5	14.8	106	2	US-10-115-123-419	Sequence 419, App

ALIGNMENTS

RESULT 1

US-08-378-617A-10

; Sequence 10, Application US/08378617A

; Patent No. 5849991

; GENERAL INFORMATION:

; APPLICANT: d'Apice, Anthony J.F.

; APPLICANT: Pearse, Martin J.

; APPLICANT: Robins, Allan J.

; APPLICANT: Crawford, Robert J.

; APPLICANT: Rathjen, Peter D.

; TITLE OF INVENTION: MATERIALS AND METHODS FOR MANAGEMENT OF

; TITLE OF INVENTION: HYPERACUTE REJECTION IN HUMAN XENOTRANSPLANTATION

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 120 South Sixth Street, Suite 2500

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30B

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/378,617A

; FILING DATE: 26-JAN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ellinger, Mark S.

; REGISTRATION NUMBER: 34,812

; REFERENCE/DOCKET NUMBER: 06868/005001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (612) 335-5070

; TELEFAX: (612) 288-9696

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 371 amino acids

SCORE Search Results Details for Application 10762888 and Search Result us-10-762-888-10.rapbm.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10762888 and Search Result us-10-762-888-10.rapbm.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2006, 05:45:23 ; Search time 185 Seconds
(without alignments)
928.934 Million cell updates/sec

Title: US-10-762-888-10
Perfect score: 2015
Sequence: 1 MNVKG RVVLSMLLVSTVMVV.....IRIVKIAWQKKEYNLVRNNI 371

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2015	100.0	371	3	US-09-994-427A-10
2	2015	100.0	371	4	US-10-105-963-8
3	2015	100.0	371	4	US-10-762-888-10
4	2015	100.0	371	5	US-10-499-407-1
5	2015	100.0	371	6	US-11-198-685-8
6	2015	100.0	371	6	US-11-198-069-8
7	2015	100.0	371	6	US-11-219-419-8
8	1726.5	85.7	376	3	US-09-994-427A-12
9	1723.5	85.5	376	3	US-09-994-427A-6
10	1723.5	85.5	376	3	US-09-995-419A-9
11	1723.5	85.5	376	4	US-10-811-012-9
12	1723.5	85.5	376	6	US-11-198-685-6
13	1723.5	85.5	376	6	US-11-198-069-6
14	1717.5	85.2	368	3	US-09-994-427A-9

15	1717.5	85.2	368	4	US-10-105-963-6	Sequence 6, Appli
16	1717.5	85.2	368	4	US-10-762-888-11	Sequence 11, Appl
17	1717.5	85.2	368	6	US-11-198-685-4	Sequence 4, Appli
18	1717.5	85.2	368	6	US-11-198-069-4	Sequence 4, Appli
19	1717.5	85.2	368	6	US-11-219-419-6	Sequence 6, Appli
20	1711	84.9	369	3	US-09-994-427A-8	Sequence 8, Appli
21	1711	84.9	369	3	US-09-995-419A-7	Sequence 7, Appli
22	1711	84.9	369	4	US-10-105-963-4	Sequence 4, Appli
23	1711	84.9	369	4	US-10-105-616-3	Sequence 3, Appli
24	1711	84.9	369	4	US-10-811-012-7	Sequence 7, Appli
25	1711	84.9	369	6	US-11-198-685-2	Sequence 2, Appli
26	1711	84.9	369	6	US-11-198-069-2	Sequence 2, Appli
27	1711	84.9	369	6	US-11-219-419-4	Sequence 4, Appli
28	1709.5	84.8	376	3	US-09-994-427A-13	Sequence 13, Appl
29	1575	78.2	371	3	US-09-870-759-74	Sequence 74, Appl
30	1575	78.2	371	3	US-09-751-708A-74	Sequence 74, Appl
31	1575	78.2	371	4	US-10-762-888-12	Sequence 12, Appl
32	1575	78.2	371	4	US-10-428-817A-70	Sequence 70, Appl
33	1575	78.2	371	5	US-10-937-758A-51	Sequence 51, Appl
34	1575	78.2	371	5	US-10-838-750-2	Sequence 2, Appli
35	1556	77.2	416	5	US-10-330-773-703	Sequence 703, App
36	1510	74.9	359	3	US-09-994-427A-11	Sequence 11, Appl
37	1510	74.9	394	3	US-09-863-475A-4	Sequence 4, Appli
38	1510	74.9	394	3	US-09-946-034-2	Sequence 2, Appli
39	1510	74.9	394	4	US-10-172-459-2	Sequence 2, Appli
40	1510	74.9	394	6	US-11-198-685-10	Sequence 10, Appl
41	1510	74.9	394	6	US-11-198-069-10	Sequence 10, Appl
42	993	49.3	227	3	US-09-994-427A-7	Sequence 7, Appli
43	752	37.3	276	5	US-10-478-519-4	Sequence 4, Appli
44	714	35.4	212	5	US-10-330-773-706	Sequence 706, App
45	697	34.6	197	6	US-11-198-685-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-994-427A-10

; Sequence 10, Application US/09994427A

; Patent No. US20020128221A1

; GENERAL INFORMATION:

; APPLICANT: Geron Corporation

; APPLICANT: Schiff, J. Michael

; TITLE OF INVENTION: GLYCOSYLTRANSFERASE VECTORS FOR TREATING CANCER

; FILE REFERENCE: 083,002

; CURRENT APPLICATION NUMBER: US/09/994,427A

; CURRENT FILING DATE: 2002-02-26

; PRIOR APPLICATION NUMBER: 60/253,395

; PRIOR FILING DATE: 2000-11-27

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 371

; TYPE: PR1

; ORGANISM: Sus scrofa

US-09-994-427A-10

Query Match 100.0%; Score 2015; DB 3; Length 371;
 Best Local Similarity 100.0%; Pred. No. 6.2e-191;
 Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVKGRVLSMLLVSTVMVFWWEYINSPEGLFWIYQSKNPEVGSSAQRGWWFPSWFNNG	60
Db	1	MNVKGRVLSMLLVSTVMVFWWEYINSPEGLFWIYQSKNPEVGSSAQRGWWFPSWFNNG	60
Qy	61	THSYHEEEDAIGNEKEQRKEDNRGELPLVDWFNPEKRPEVVTITRWKAPVWEGTYNRAV	120
Db	61	THSYHEEEDAIGNEKEQRKEDNRGELPLVDWFNPEKRPEVVTITRWKAPVWEGTYNRAV	120
Qy	121	LDNYAKQKITVGLTVFAVGRIEYHLEEFISANTYFMVGHKVIFYIMVDDISRMPLIE	180
Db	121	LDNYAKQKITVGLTVFAVGRIEYHLEEFISANTYFMVGHKVIFYIMVDDISRMPLIE	180
Qy	181	LGPLRSFKVFEIKSEKRWQDISMMRMKTIGEHLAHIQHEVDVDFCMDVDQVFQNNFGVE	240
Db	181	LGPLRSFKVFEIKSEKRWQDISMMRMKTIGEHLAHIQHEVDVDFCMDVDQVFQNNFGVE	240

SCORE Search Results Details for Application 10762888 and Search Result us-10-762-888-10.rapbn.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10762888 and Search Result us-10-762-888-10.rapbn.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2006, 05:46:38 ; Search time 43 Seconds
(without alignments)
737.535 Million cell updates/sec

Title: US-10-762-888-10
Perfect score: 2015
Sequence: 1 MNVKG RVLSMLLVSTVMVV.....IRIVKIAWQKKEYNLVRNNI 371

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 330775 seqs, 85482512 residues

Total number of hits satisfying chosen parameters: 330775

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1723.5	85.5	376	7	US-11-355-804-3	Sequence 3, Appli
2	1556	77.2	416	6	US-10-540-898-703	Sequence 703, App
3	714	35.4	212	6	US-10-540-898-706	Sequence 706, App
4	644.5	32.0	347	7	US-11-375-359-113	Sequence 113, App
5	638.5	31.7	354	7	US-11-388-595-137	Sequence 137, App
6	102.5	5.1	449	7	US-11-330-403-18486	Sequence 18486, A
7	102.5	5.1	453	7	US-11-330-403-17399	Sequence 17399, A
8	93.5	4.6	441	7	US-11-330-403-3112	Sequence 3112, Ap
9	89.5	4.4	380	7	US-11-343-271-5	Sequence 5, Appli
10	89	4.4	763	6	US-10-449-902-52890	Sequence 52890, A
11	88	4.4	398	6	US-10-526-324-1037	Sequence 1037, Ap
12	86.5	4.3	311	7	US-11-316-042-224	Sequence 224, App

13	86.5	4.3	311	7	US-11-316-042-225	Sequence 225, App
14	86.5	4.3	311	7	US-11-316-042-226	Sequence 226, App
15	86.5	4.3	311	7	US-11-316-042-227	Sequence 227, App
16	86.5	4.3	1406	7	US-11-263-326-171	Sequence 171, App
17	86.5	4.3	1406	7	US-11-262-647-171	Sequence 171, App
18	86.5	4.3	1532	7	US-11-365-989-226	Sequence 226, App
19	86.5	4.3	1795	7	US-11-263-326-124	Sequence 124, App
20	86.5	4.3	1795	7	US-11-262-647-124	Sequence 124, App
21	86.5	4.3	1855	7	US-11-263-326-125	Sequence 125, App
22	86.5	4.3	1855	7	US-11-262-647-125	Sequence 125, App
23	86.5	4.3	1891	7	US-11-263-326-173	Sequence 173, App
24	86.5	4.3	1891	7	US-11-262-647-173	Sequence 173, App
25	86.5	4.3	2009	7	US-11-263-326-2	Sequence 2, Appli
26	86.5	4.3	2009	7	US-11-263-326-4	Sequence 4, Appli
27	86.5	4.3	2009	7	US-11-263-326-6	Sequence 6, Appli
28	86.5	4.3	2009	7	US-11-263-326-10	Sequence 10, Appl
29	86.5	4.3	2009	7	US-11-263-326-12	Sequence 12, Appl
30	86.5	4.3	2009	7	US-11-263-326-121	Sequence 121, App
31	86.5	4.3	2009	7	US-11-263-326-122	Sequence 122, App
32	86.5	4.3	2009	7	US-11-263-326-123	Sequence 123, App
33	86.5	4.3	2009	7	US-11-263-326-126	Sequence 126, App
34	86.5	4.3	2009	7	US-11-263-326-127	Sequence 127, App
35	86.5	4.3	2009	7	US-11-263-326-167	Sequence 167, App
36	86.5	4.3	2009	7	US-11-263-326-168	Sequence 168, App
37	86.5	4.3	2009	7	US-11-263-326-169	Sequence 169, App
38	86.5	4.3	2009	7	US-11-263-326-170	Sequence 170, App
39	86.5	4.3	2009	7	US-11-263-326-172	Sequence 172, App
40	86.5	4.3	2009	7	US-11-262-647-2	Sequence 2, Appli
41	86.5	4.3	2009	7	US-11-262-647-4	Sequence 4, Appli
42	86.5	4.3	2009	7	US-11-262-647-6	Sequence 6, Appli
43	86.5	4.3	2009	7	US-11-262-647-10	Sequence 10, Appl
44	86.5	4.3	2009	7	US-11-262-647-12	Sequence 12, Appl
45	86.5	4.3	2009	7	US-11-262-647-121	Sequence 121, App

ALIGNMENTS

RESULT 1

```

US-11-355-804-3
; Sequence 3, Application US/11355804
; Publication No. US20060251661A1
; GENERAL INFORMATION:
; APPLICANT: Galili, Uri
; TITLE OF INVENTION: Tumor Lesion Regression and Conversion In Situ into Autologous
; TITLE OF INVENTION: Tumor Vaccines by Compositions that Result in Anti-Gal Antibody
; TITLE OF INVENTION: Binding
; FILE REFERENCE: UMASSW-10253
; CURRENT APPLICATION NUMBER: US/11/355,804
; CURRENT FILING DATE: 2006-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Callithrix jacchus
US-11-355-804-3

```

Query Match 85.5%; Score 1723.5; DB 7; Length 376;
Best Local Similarity 82.2%; Pred. No. 3.8e-149;
Matches 309; Conservative 34; Mismatches 28; Indels 5; Gaps 2;

[illegible]

SCORE Search Results Details for Application 10762888 and Search Result us-10-762-888-10.rapm.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10762888 and Search Result us-10-762-888-10.rapm.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2006, 05:33:58 ; Search time 613 Seconds
(without alignments)
924.145 Million cell updates/sec

Title: US-10-762-888-10
Perfect score: 2015
Sequence: 1 MNVKGRRVLSMLLVSTVMVV.....IRIVKIAWQKKEYNLVRNNI 371

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/paa/PCTUS_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/paa/US066_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/paa/US073_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/paa/US074_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/paa/US075_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/paa/US076_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/paa/US077_COMB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/paa/US078_COMB.pep:*
9: /EMC_Celerra_SIDS3/ptodata/2/paa/US079_COMB.pep:*
10: /EMC_Celerra_SIDS3/ptodata/2/paa/US080_COMB.pep:*
11: /EMC_Celerra_SIDS3/ptodata/2/paa/US081_COMB.pep:*
12: /EMC_Celerra_SIDS3/ptodata/2/paa/US082_COMB.pep:*
13: /EMC_Celerra_SIDS3/ptodata/2/paa/US083_COMB.pep:*
14: /EMC_Celerra_SIDS3/ptodata/2/paa/US084_COMB.pep:*
15: /EMC_Celerra_SIDS3/ptodata/2/paa/US085_COMB.pep:*
16: /EMC_Celerra_SIDS3/ptodata/2/paa/US086_COMB.pep:*
17: /EMC_Celerra_SIDS3/ptodata/2/paa/US087_COMB.pep:*
18: /EMC_Celerra_SIDS3/ptodata/2/paa/US088_COMB.pep:*
19: /EMC_Celerra_SIDS3/ptodata/2/paa/US089_COMB.pep:*
20: /EMC_Celerra_SIDS3/ptodata/2/paa/US090_COMB.pep:*
21: /EMC_Celerra_SIDS3/ptodata/2/paa/US091_COMB.pep:*
22: /EMC_Celerra_SIDS3/ptodata/2/paa/US092_COMB.pep:*
23: /EMC_Celerra_SIDS3/ptodata/2/paa/US093_COMB.pep:*
24: /EMC_Celerra_SIDS3/ptodata/2/paa/US094_COMB.pep:*
25: /EMC_Celerra_SIDS3/ptodata/2/paa/US095_COMB.pep:*
26: /EMC_Celerra_SIDS3/ptodata/2/paa/US096_COMB.pep:*
27: /EMC_Celerra_SIDS3/ptodata/2/paa/US097_COMB.pep:*
28: /EMC_Celerra_SIDS3/ptodata/2/paa/US098_COMB.pep:*
29: /EMC_Celerra_SIDS3/ptodata/2/paa/US099_COMB.pep:*
30: /EMC_Celerra_SIDS3/ptodata/2/paa/US100_COMB.pep:*

31: /EMC_Celerra_SIDS3/ptodata/2/paa/US101_COMB.pep:*
 32: /EMC_Celerra_SIDS3/ptodata/2/paa/US102_COMB.pep:*
 33: /EMC_Celerra_SIDS3/ptodata/2/paa/US103_COMB.pep:*
 34: /EMC_Celerra_SIDS3/ptodata/2/paa/US104_COMB.pep:*
 35: /EMC_Celerra_SIDS3/ptodata/2/paa/US105_COMB.pep:*
 36: /EMC_Celerra_SIDS3/ptodata/2/paa/US106_COMB.pep:*
 37: /EMC_Celerra_SIDS3/ptodata/2/paa/US107_COMB.pep:*
 38: /EMC_Celerra_SIDS3/ptodata/2/paa/US108_COMB.pep:*
 39: /EMC_Celerra_SIDS3/ptodata/2/paa/US109_COMB.pep:*
 40: /EMC_Celerra_SIDS3/ptodata/2/paa/US110_COMB.pep:*
 41: /EMC_Celerra_SIDS3/ptodata/2/paa/US111_COMB.pep:*
 42: /EMC_Celerra_SIDS3/ptodata/2/paa/US112_COMB.pep:*
 43: /EMC_Celerra_SIDS3/ptodata/2/paa/US113_COMB.pep:*
 44: /EMC_Celerra_SIDS3/ptodata/2/paa/US114_COMB.pep:*
 45: /EMC_Celerra_SIDS3/ptodata/2/paa/US600_COMB.pep:*
 46: /EMC_Celerra_SIDS3/ptodata/2/paa/US601_COMB.pep:*
 47: /EMC_Celerra_SIDS3/ptodata/2/paa/US602_COMB.pep:*
 48: /EMC_Celerra_SIDS3/ptodata/2/paa/US603_COMB.pep:*
 49: /EMC_Celerra_SIDS3/ptodata/2/paa/US604_COMB.pep:*
 50: /EMC_Celerra_SIDS3/ptodata/2/paa/US605_COMB.pep:*
 51: /EMC_Celerra_SIDS3/ptodata/2/paa/US606_COMB.pep:*
 52: /EMC_Celerra_SIDS3/ptodata/2/paa/US607_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2015	100.0	371	1	PCT-US02-41287-1	Sequence 1, Appli
2	2015	100.0	371	1	PCT-US03-03059-2	Sequence 2, Appli
3	2015	100.0	371	25	US-09-593-316-8	Sequence 8, Appli
4	2015	100.0	371	31	US-10-105-963-8	Sequence 8, Appli
5	2015	100.0	371	34	US-10-499-407-1	Sequence 1, Appli
6	2015	100.0	371	37	US-10-762-888-10	Sequence 10, Appl
7	2015	100.0	371	41	US-11-198-069-8	Sequence 8, Appli
8	2015	100.0	371	41	US-11-198-685-8	Sequence 8, Appli
9	2015	100.0	371	42	US-11-219-419-8	Sequence 8, Appli
10	2009	99.7	375	22	US-09-230-091-2	Sequence 2, Appli
11	1998	99.2	371	11	US-08-188-607B-10	Sequence 10, Appl
12	1998	99.2	371	13	US-08-378-617-10	Sequence 10, Appl
13	1923	95.4	363	22	US-09-230-091-4	Sequence 4, Appli
14	1858.5	92.2	354	22	US-09-230-091-6	Sequence 6, Appli
15	1779.5	88.3	342	22	US-09-230-091-8	Sequence 8, Appli
16	1723.5	85.5	376	12	US-08-213-200A-2	Sequence 2, Appli
17	1723.5	85.5	376	25	US-09-593-316-6	Sequence 6, Appli
18	1723.5	85.5	376	38	US-10-811-012-9	Sequence 9, Appli
19	1723.5	85.5	376	41	US-11-198-069-6	Sequence 6, Appli
20	1723.5	85.5	376	41	US-11-198-685-6	Sequence 6, Appli
21	1717.5	85.2	368	11	US-08-188-607B-11	Sequence 11, Appl
22	1717.5	85.2	368	13	US-08-378-617-11	Sequence 11, Appl
23	1717.5	85.2	368	25	US-09-593-316-4	Sequence 4, Appli
24	1717.5	85.2	368	31	US-10-105-963-6	Sequence 6, Appli
25	1717.5	85.2	368	37	US-10-762-888-11	Sequence 11, Appl
26	1717.5	85.2	368	41	US-11-198-069-4	Sequence 4, Appli
27	1717.5	85.2	368	41	US-11-198-685-4	Sequence 4, Appli
28	1717.5	85.2	368	42	US-11-219-419-6	Sequence 6, Appli
29	1711	84.9	369	25	US-09-593-316-2	Sequence 2, Appli
30	1711	84.9	369	31	US-10-105-616-3	Sequence 3, Appli
31	1711	84.9	369	31	US-10-105-963-4	Sequence 4, Appli
32	1711	84.9	369	38	US-10-811-012-7	Sequence 7, Appli
33	1711	84.9	369	41	US-11-198-069-2	Sequence 2, Appli
34	1711	84.9	369	41	US-11-198-685-2	Sequence 2, Appli
35	1711	84.9	369	42	US-11-219-419-4	Sequence 4, Appli
36	1575	78.2	371	11	US-08-188-607B-12	Sequence 12, Appl
37	1575	78.2	371	13	US-08-378-617-12	Sequence 12, Appl
38	1575	78.2	371	27	US-09-751-708A-74	Sequence 74, Appl
39	1575	78.2	371	28	US-09-870-759-74	Sequence 74, Appl
40	1575	78.2	371	34	US-10-428-817A-70	Sequence 70, Appl
41	1575	78.2	371	37	US-10-762-888-12	Sequence 12, Appl
42	1575	78.2	371	38	US-10-838-750-2	Sequence 2, Appli
43	1575	78.2	371	39	US-10-937-758A-51	Sequence 51, Appl
44	1556	77.2	416	33	US-10-330-773-703	Sequence 703, App

SCORE Search Results Details for Application 10762888 and Search Result us-10-762-888-10.rapn.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10762888 and Search Result us-10-762-888-10.rapn.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2006, 05:34:58 ; Search time 76 Seconds
(without alignments)
828.334 Million cell updates/sec

Title: US-10-762-888-10
Perfect score: 2015
Sequence: 1 MNVKGRVLSMLLVSTVMVV.....IRIVKIAWQKKEYNLVRNNI 371

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 739873 seqs, 169685768 residues

Total number of hits satisfying chosen parameters: 739873

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/paa/PCT_NEW_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/paa/US11_NEW_COMB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1723.5	85.5	376	7	US-11-355-804-3
2	1575	78.2	371	1	PCT-US06-11960-455
3	1556	77.2	416	1	PCT-US03-41389-703
4	714	35.4	212	1	PCT-US03-41389-706
5	643.5	31.9	354	8	US-60-812-076-56
6	642.5	31.9	347	7	US-11-371-354-62137
7	638.5	31.7	354	1	PCT-US06-11065-137
8	638.5	31.7	354	7	US-11-388-595-137
9	638.5	31.7	354	8	US-60-812-076-54
10	627.5	31.1	391	8	US-60-812-076-53
11	627.5	31.1	391	8	US-60-812-076-55
12	531	26.4	167	1	PCT-US06-33148-5586

ALIGNMENTS

US-11-355-804-3

<http://es/ScoreAccessWeb/GetItem.action?AppId=10762888&seqId=828820&ItemName=us-10-762-888-10.rapn...> 11/20/06

SCORE Search Results Details for A

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10762888 and Search Result us-10-762-888-10.rpr.
[start](#)

GenCore version 5.1.9

Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2006, 05:28:02 ; Search time 43 Seconds
(without alignments)
830.149 Million cell updates/sec

Title: US-10-762-888-10
Perfect score: 2015
Sequence: 1 MNVKGRVLSMLLVSTVMVV.....IRIVKIAWQKKEYNLVRNNI 371

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pirl1:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2015	100.0	371	2	I46583
2	1717.5	85.2	368	2	A44785
3	1717.5	85.2	376	2	A56480
4	1575	78.2	371	2	I49698
5	1510	74.9	394	2	A34417
6	640	31.8	295	2	PC1120
7	639	31.7	353	1	A34933
8	625	31.0	347	2	JC6126
9	456	22.6	189	2	PC1168
10	452	22.4	189	2	PC1166
11	451	22.4	189	2	PC1165
12	446	22.1	189	2	PC1173
13	443	22.0	189	2	PC1170
14	443	22.0	189	2	PC1169
15	443	22.0	189	2	PC1171
16	441	21.9	189	2	PC1172
17	113	5.6	26	2	A39769
18	100	5.0	522	2	AB2928
19	100	5.0	522	2	E98354
20	96.5	4.8	569	2	A43317
					alpha-1,3-galactos
					N-acetyllactosamin
					N-acetyllactosamin
					alpha-1,3-galactos
					alpha-1,3-mannosyl
					glycoprotein-fucos
					glycoprotein-fucos
					globoside alpha-N-
					histo-blood group
					histo-blood group
					glycoprotein-fucos
					histo-blood group
					histo-blood group
					histo-blood group
					histo-blood group
					histo-blood group
					N-acetyllactosamin
					hypothetical prote
					algQ1 (AB011415) {
					germ cell-less pro

21	95.5	4.7	1503	2	T18266	cycloinulo-oligosa
22	94.5	4.7	1520	2	B82274	conserved hypothet
23	93.5	4.6	275	2	E90580	conserved hypothet
24	93.5	4.6	384	2	E75095	hypothetical prote
25	93.5	4.6	441	2	F81667	glucose-1-phosphat
26	93	4.6	1827	1	UUHU	sucrose alpha-gluc
27	92.5	4.6	278	2	F86679	hypothetical prote
28	92.5	4.6	546	2	T23920	hypothetical prote
29	91.5	4.5	549	2	S44188	alpha-glucosidase
30	91.5	4.5	689	2	C84192	methionine-tRNA sy
31	91	4.5	901	2	C96696	protein FlN21.6 [i
32	90.5	4.5	260	2	AB2094	hypothetical prote
33	90.5	4.5	678	2	T32483	hypothetical prote
34	90.5	4.5	724	2	C49423	semaphorin II prec
35	90.5	4.5	1086	2	AF1662	cellobiose-phospho
36	90.5	4.5	1153	2	B97718	hypothetical prote
37	90	4.5	196	2	D83829	hypothetical prote
38	89.5	4.4	274	2	D97141	probable aldo/keto
39	89.5	4.4	438	2	AD0389	phosphate regulon
40	89	4.4	393	2	S61659	KTR1 protein - yea
41	89	4.4	722	2	AF1421	hypothetical membr
42	88	4.4	692	2	T41240	hypothetical zinc
43	88	4.4	2054	2	T07584	hypothetical prote
44	87.5	4.3	296	2	AI1178	transcription regu
45	87.5	4.3	455	2	T29555	hypothetical prote

ALIGNMENTS

RESULT 1

I46583

alpha-1,3-galactosyltransferase - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004

C;Accession: I46583

R;Strahan, K.M.; Gu, F.; Preece, A.F.; Gustavsson, I.; Andersson, L.; Gustafsson, K. Immunogenetics 41, 101-105, 1995

A;Title: cDNA sequence and chromosome localization of pig alpha 1,3 galactosyltransferase.

A;Reference number: I46583; MUID:95104914; PMID:7528726

A;Accession: I46583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-371

A;Cross-references: UNIPROT:P50127; UNIPARC:UPI00000009A4; GB:L36152; NID:g642635; PIDN:AAA73558.1; PID:g642636

C;Genetics:

A;Gene: GGTA1

C;Superfamily: histo-blood group 1 transferase

Query Match 100.0%; Score 2015; DB 2; Length 371;
 Best Local Similarity 100.0%; Pred. No. 1.3e-162;
 Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MNVKGRVVL SMLLVSTVMVFW EYINSPEGSLFWIYQSKNPEVGSSAQRGWWFPSWFNNG 60
         |||
Db      1 MNVKGRVVL SMLLVSTVMVFW EYINSPEGSLFWIYQSKNPEVGSSAQRGWWFPSWFNNG 60

Qy     61 THSYHEEEDAIGNEKEQRKEDNRGELPLVDWFNPEKRPEVVTITRWKAPVVWEGTYNRAV 120
         |||
Db     61 THSYHEEEDAIGNEKEQRKEDNRGELPLVDWFNPEKRPEVVTITRWKAPVVWEGTYNRAV 120

Qy    121 LDNYAKQKITVGLTVFAVGRIEYHYLEEFLISANTYFMVGHKVIFYIMVDDISRMLPIE 180
         |||
Db    121 LDNYAKQKITVGLTVFAVGRIEYHYLEEFLISANTYFMVGHKVIFYIMVDDISRMLPIE 180

Qy    181 LGPLRSFKVFEIKSEKRWQDISMMRMKTIGEHLAHIQHEVDVDFLCMDVDQVFQNNFGVE 240
         |||
Db    181 LGPLRSFKVFEIKSEKRWQDISMMRMKTIGEHLAHIQHEVDVDFLCMDVDQVFQNNFGVE 240

Qy    241 TLGQSAQLQAWWYKAHPDEFTYERRKESAAYIPFGQGDFYHAAIFGGTPTQVLNITQE 300
         |||
Db    241 TLGQSAQLQAWWYKAHPDEFTYERRKESAAYIPFGQGDFYHAAIFGGTPTQVLNITQE 300

Qy    301 CFKGILQDKENDIEAEWHDESHLNKYFLLNKPTKILSPEYCWVDYHIGMSVDIRIVKIAWQ 360
         |||
Db    301 CFKGILQDKENDIEAEWHDESHLNKYFLLNKPTKILSPEYCWVDYHIGMSVDIRIVKIAWQ 360

```

SCORE Search Results Details for Application 10762888 and Search Result us-10-762-888-10.rup.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10762888 and Search Result us-10-762-888-10.rup.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2006, 05:24:32 ; Search time 303 Seconds
(without alignments)
1132.610 Million cell updates/sec

Title: US-10-762-888-10
Perfect score: 2015
Sequence: 1 MNVKG RVVLSMLLVSTVMV.....IRIVKIAWQKKEYNLVRNNI 371

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2015	100.0	371	1	GGTA1_PIG P50127 sus scrofa
2	2015	100.0	371	2	Q548W5_PIG Q548w5 sus scrofa
3	1770.5	87.9	370	2	Q8HY56_FELCA Q8hy56 felis silve
4	1754	87.0	375	2	Q8SPR2_CEBAP Q8spr2 cebus apell
5	1735.5	86.1	376	2	Q8SQ20_CALJA Q8sq20 callithrix
6	1723.5	85.5	376	2	Q28855_9PRIM Q28855 platyrrhini
7	1717.5	85.2	368	1	GGTA1_BOVIN P14769 bos taurus
8	1714	85.1	369	2	Q6SVU1_SHEEP Q6svu1 ovis aries
9	1585	78.7	371	2	Q80WF5_RAT Q80wf5 rattus norv
10	1578	78.3	406	2	Q9DBU1_MOUSE Q9dbu1 mus musculu
11	1510	74.9	394	1	GGTA1_MOUSE P23336 mus musculu
12	1510	74.9	394	2	Q3TXW0_MOUSE Q3txw0 mus musculu
13	1475	73.2	384	2	Q8C2H7_MOUSE Q8c2h7 mus musculu
14	1423	70.6	371	2	Q8K3Z1_RAT Q8k3z1 rattus norv
15	1414	70.2	372	2	Q91W00_MOUSE Q91w00 mus musculu
16	1092	54.2	217	2	Q8HYB2_LEMCA Q8hyb2 lemur catta
17	951	47.2	332	2	Q3L7L9_RAT Q3l7l9 rattus norv
18	827	41.0	308	2	Q4R5T7_MACFA Q4r5t7 macaca fasc

19	817	40.5	308	2	Q9BH00_MACFA	Q9bh00 macaca fasc
20	808	40.1	308	2	Q7Z4J2_HUMAN	Q7z4j2 homo sapien
21	794.5	39.4	308	2	Q2YDM8_BOVIN	Q2ydm8 bos taurus
22	778	38.6	319	2	Q9D4R9_MOUSE	Q9d4r9 mus musculu
23	776.5	38.5	321	2	Q3L7M0_RAT	Q3l7m0 rattus norv
24	774	38.4	291	2	Q4RX56_TETNG	Q4rx56 tetraodon n
25	774	38.4	311	2	Q2NKH9_MOUSE	Q2nkh9 mus musculu
26	752	37.3	276	2	Q5T6T3_HUMAN	Q5t6t3 homo sapien
27	725	36.0	144	2	Q8SPX9_SHEEP	Q8spx9 ovis aries
28	724	35.9	370	2	Q3V1N9_MOUSE	Q3v1n9 mus musculu
29	678	33.6	332	2	Q5T0B8_HUMAN	Q5t0b8 homo sapien
30	661.5	32.8	343	1	GBGT1_CHICK	Q5zlk4 gallus gall
31	644.5	32.0	347	1	GBGT1_HUMAN	Q8n5d6 homo sapien
32	644	32.0	274	2	Q9UQ65_HUMAN	Q9uq65 homo sapien
33	643.5	31.9	345	2	Q70V39_HUMAN	Q70v39 homo sapien
34	643.5	31.9	354	2	Q45FB1_HUMAN	Q45fb1 homo sapien
35	643.5	31.9	361	2	Q2VU69_HUMAN	Q2vu69 homo sapien
36	641.5	31.8	344	2	Q70V33_HUMAN	Q70v33 homo sapien
37	640	31.8	295	2	Q7LCZ1_HUMAN	Q7lcz1 homo sapien
38	639.5	31.7	344	2	Q70V24_HUMAN	Q70v24 homo sapien
39	638.5	31.7	344	2	Q70V27_HUMAN	Q70v27 homo sapien
40	638.5	31.7	344	2	Q70V41_HUMAN	Q70v41 homo sapien
41	638.5	31.7	354	1	BGAT_HUMAN	P16442 h histo-blo
42	638.5	31.7	354	2	Q53I57_HUMAN	Q53i57 homo sapien
43	638.5	31.7	354	2	Q6ISD4_HUMAN	Q6isd4 homo sapien
44	637.5	31.6	334	2	Q8CFC4_RAT	Q8cfc4 rattus norv
45	637.5	31.6	353	2	Q6IS73_HUMAN	Q6is73 homo sapien

ALIGNMENTS

RESULT 1

GGTA1_PIG

ID GGTAl_PIG STANDARD; PRT; 371 AA.
AC P50127;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 38.
DE N-acetyllactosaminide alpha-1,3-galactosyltransferase (EC 2.4.1.87)
DE (Galactosyltransferase) (UDP-galactose:beta-D-galactosyl-1,4-N-acetyl-
DE D-glucosaminide alpha-1,3-galactosyltransferase).
GN Name=GGTA1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Yorkshire; TISSUE=Spleen;
RX MEDLINE=95104914; PubMed=7528726; DOI=10.1007/BF00182319;
RA Strahan K.M., Gu F., Preece A.F., Gustavsson I., Andersson L.,
RA Gustafsson K.;
RT "cDNA sequence and chromosome localization of pig alpha 1,3
RT galactosyltransferase.";
RL Immunogenetics 41:101-105(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Liver, and Spleen;
RA Sandrin M.S., Dabkowski P.L., Henning M.M., Mouhtouris E.,
RA McKenzie I.F.C.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Transfer of galactose from UDP-galactose to an acceptor
CC molecule (R).
CC -!- CATALYTIC ACTIVITY: UDP-galactose + beta-D-galactosyl-(1->4)-beta-
CC N-acetyl-D-glucosaminyl-R = UDP + alpha-D-galactosyl-(1->3)-beta-
CC D-galactosyl-(1->4)-beta-N-acetylglucosaminyl-R.
CC -!- COFACTOR: Manganese.
CC -!- PATHWAY: Glycosylation.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Membrane-bound
CC form in trans cisternae of Golgi.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P50127-1; Sequence=Displayed;